

```

1  CCCTTTAAAG AGGGCTTTTA TATATTAATC ACAAATCACT TATGACAAAT
51  CACAAGTGAT TTGTGATTGT TGATGATAAA ATAAGAATAA GAAGAAATAG
101 AAAGAAGTGA GTGATTGTGG GAAATTTAGG CGCACAAAAA GAAAGAGTGT
                                     -35
151 GACAAAACAT GGTTATGCTA CATGTTTAAG GTAAAAATAG TTATGTCACA
                                     -10
201 ACTACTTATT TTTTACCCA ATCTTCTAGA CTATAATTAA AATTAAATAA
                                     XbaI
                                     M T I P D A N A I Y
251 CTCAATTCTGG AGGTACTAAC ATGACTATAC CTGACGCAA TGCAATCTAT
                                     RBS START
                                     H N S A I K E V V F I K N V I K S
301 CATAACTCAG CCATCAAAGA GGTGTCTTT ATCAAGAACG TGATCAAAAG
                                     DdeI DpnI
                                     P N I E I G D Y T Y Y D D P V N
351 TCCCAATATT GAAATTGGGG ACTACACCTA TTATGATGAC CCAGTAAATC
                                     SspI
                                     P T D F E K H V T H H Y E F L G D
401 CCACCGATTT TGAGAAACAC GTTACCCATC ACTATGAATT TCTAGGCGAC
                                     K L I I G K F C S L A S G I E F I
451 AAATTAATCA TCGGTAAATT TTGTTCTCTC GCCAGTGGCA TTGAATTTAT
                                     M N G A N H V M K G I S T Y P F
501 CATGAACGGT GCCAACCACG TAATGAAAGG TATTTCTGACT TATCCATTTA
                                     TaqI
                                     N I L G G D W Q Q Y T P E L T D L
551 ATATATTAGG TGGCGATTGG CAACAATACA CTCCTGAACT GACTGATTTG
                                     P L K G T V V G N D V W F G Q N V
601 CCGTTGAAAG GTGATACTGT AGTCGGAAAT GACGTGTGGT TTGGGCAAAA
                                     T V L P G V K I G D G A I I G A
651 TGTGACCGTC CTACCAGGCG TAAAAATAGG TGACGGTGCC ATTATCGGAG
                                     N S V V T K D V A P Y T I V G G N
701 CAAATAGTGT TGTAACAAAA GACGTCGCTC CATATACAAT TGTCGGTGGC
                                     P I Q L I G P R F E P E V I Q A L
751 AATCCAATTC AACTCATCGG ACCAAGATTT GAACCGGAAG TTATCAAGC
                                     XmnI
                                     E N L A W W N K D I E W I T A N
801 ATTAGAAAAT CTGGCATGGT GGAATAAAGA TATTGAATGG ATAACTGCTA
                                     N V P K L M Q T T P T L E L I N S
851 ATGTTCTTAA ACTAATGCAA ACAACACCCA CACTTGAATT GATAAACAGT
                                     L M E K *
                                     STOP
901 TTAATGGAAA AATAAAAAACA AAAAAGCCGT GCAAGCAATC CAAAAATGAT
951 TGTTTACACG GCCTTTACTA TTAGTGAAT CCAATTTATT AATAATAGAT
                                     HaeIII
1001 ATGATATACC AGTAAAAAAT AACTAGCCA CCTCTGGCGG TACTCTACTC
1051 GTATATTTTA TTTACGACCT TCTGATGATA

```

FIGURE 1

[illegible]

YEVIGDKLIGRFGSIGPGTTFIMNGANHMDG-STYPFHLMRGWEKYMPSLKDLPLKG
YELIGDKLILGKFGSIGPGTTFIMNGANHMDG-STEPFNLFNGWEKHPTLEDLPYKG
YPLINDKLIGKFGSIGPGVTIIMNGANHMDG-STYPFNLFNGWEKHPKLDQLPIKG
YEFRGDKLVIGKFCIAEGIEFIMNGANHMRNSITTYPFNIMGNGWEKATPSLEDLPFKG
YEFLGDKLIGKFGCSLASGIEFIMNGANHVMKGISTYPFNILGGDWQYTPELTDLPLKG
* * * * * : * * * * * : * * * * * : * * * * * : * * * * *

[illegible]

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IEEWLALQWNLDMKIIENENLPFIING--DIEMLKRRKRLDDPT
IALALKVRWMDLEIETINENIDCILNG--DIKKVRS-----
INOLLDIKWWNPIDIENENIDKILDN--SIIREVIWKK-----
IDYLLQIKWWDWSAQKIFSNLETCCS--DLEKIKSIRD-----
IQALENLAWWNKDIEWITANVPKLMQTTPTLELINSLMEK----
*      *      *      *      *      *      *

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FIGURE 2

1080 bp : restriction map

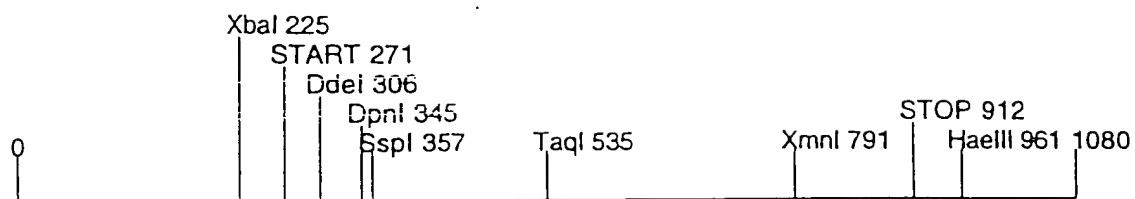


FIGURE3